

SEQUENCE LISTING

<110> Rothschild, Max
Ciobanu, Dan
Malek, Massoud
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

<130> P04668US3

<150> 60/231045

<151> 2000-09-08

<150> 60/260,239

<151> 2001-01-08

<150> 60/299,111

<151> 2001-06-18

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 1873

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (1) .. (1392)

<400> 1

atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

48

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

96

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

144

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

192

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

340

gcc gag gtg gac aac ccc cca aca gag cg^g gac atc ctc ccc tct gac
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 86 87 88 89 90 91 92 93 94 95

200

032501222 - 03251201

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc		336	
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
100	105	110	
ata gag ttc tca gcc tcg gcg tcg ggg gat gag ctt ggg ctg gtg		384	
Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val			
115	120	125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg		432	
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg			
130	135	140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg		480	
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met			
145	150	155	160
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc		528	
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser			
165	170	175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt		576	
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe			
180	185	190	
gcc ctg gtg gcc aac ggc gtc cga gcg gca cct ttg tgg gac agc aag		624	
Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys			
195	200	205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg		672	
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val			
210	215	220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa		720	
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu			
225	230	235	240
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc		768	
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe			
245	250	255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc		816	
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val			
260	265	270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct		864	
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro			
275	280	285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag		912	
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys			
290	295	300	
ttc ctg cac atc ttt ggc acc ctg ccc ccg ccc tcc ttc ctc tac		960	
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr			
305	310	315	320
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg		1008	
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val			
325	330	335	

卷之三

<210> 2
<211> 464
<212> PRT
<213> Sus scrofa

<400> 2

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190 *

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

卷之三

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
450 455 460

<210> 3
<211> 1873

<212> DNA
<213> Sus scrofa

<220>
<221> CDS
<222> (1) .. (1392)

<400> 3																		
atg	agc	ttc	cta	gag	caa	gga	gag	agc	cgt	tca	tgg	cca	tcc	cga	gct		48	
Met	Ser	Phe	Leu	Glu	Gln	Gly	Glu	Ser	Arg	Ser	Trp	Pro	Ser	Arg	Ala			
1																15		
10																		
gta	acc	acc	agc	tca	gaa	aga	aga	agc	cat	ggg	gac	cag	ggg	acc	aag	gcc		96
Val	Thr	Thr	Ser	Ser	Glu	Arg	Ser	His	Gly	Asp	Gln	Gly	Thr	Lys	Ala			
20																	30	
25																		
tct	aga	tgg	aca	agg	cag	gag	gat	gta	gag	gaa	ggg	ggg	cct	ccg	ggc		144	
Ser	Arg	Trp	Thr	Arg	Gln	Glu	Asp	Val	Glu	Gly	Gly	Gly	Pro	Pro	Gly			
35																	45	
40																		
ccg	agg	gaa	ggt	ccc	cag	tcc	agg	cca	gtt	gct	gag	tcc	acc	ggg	cag		192	
Pro	Arg	Glu	Gly	Pro	Gln	Ser	Arg	Pro	Val	Ala	Glu	Ser	Thr	Gly	Gln			
50																	60	
55																		
gag	gcc	aca	ttc	ccc	aag	gcc	aca	ccc	ttg	gcc	caa	gcc	gct	ccc	ttg		240	
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu			
65																	80	
70																		
gcc	gag	gtg	gac	aac	ccc	cca	aca	gag	cg	gac	atc	ctc	ccc	tct	gac		288	
Ala	Glu	Val	Asp	Asn	Pro	Pro	Thr	Glu	Arg	Asp	Ile	Leu	Pro	Ser	Asp			
85																	95	
90																		
tgt	gca	gcc	tca	gcc	tcc	gac	tcc	aac	aca	gac	cat	ctg	gat	ctg	ggc		336	
Cys	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Asn	Thr	Asp	His	Leu	Asp	Leu	Gly			
100																	110	
105																		
ata	gag	ttc	tca	gcc	tcg	gcg	tcg	ggg	gat	gag	ctt	ggg	ctg	gtg			384	
Ile	Glu	Phe	Ser	Ala	Ser	Ala	Ala	Ser	Gly	Asp	Glu	Leu	Gly	Leu	Val			
115																	125	
120																		
gaa	gag	aag	cca	gcc	ccg	tgc	cca	tcc	cca	gag	gtg	ctg	tta	ccc	agg		432	
Glu	Glu	Lys	Pro	Ala	Pro	Cys	Pro	Ser	Pro	Glu	Val	Leu	Leu	Pro	Arg			
130																	140	
135																		
ctg	ggc	tgg	gat	gat	gag	ctg	cag	aag	ccg	ggg	gcc	cag	gtc	tac	atg		480	
Leu	Gly	Trp	Asp	Asp	Glu	Leu	Gln	Lys	Pro	Gly	Ala	Gln	Val	Tyr	Met			
145																	160	
150																		
cac	tcc	atg	cag	gag	cac	acc	tgc	tac	gat	gcc	atg	gcg	acc	agc	tcc		528	
His	Phe	Met	Gln	Glu	His	Thr	Cys	Tyr	Asp	Ala	Met	Ala	Thr	Ser	Ser			
165																	175	
170																		
aaa	ctg	gtc	atc	ttc	gac	acc	atg	ctg	gag	atc	aag	aag	gcc	ttc	ttt		576	
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe			
180																	190	
185																		
gcc	ctg	gtg	gcc	aac	ggc	gtc	cga	gca	cct	ttg	tgg	gac	agc	aag			624	
Ala	Leu	Val	Ala	Asn	Gly	Val	Arg	Ala	Ala	Pro	Leu	Trp	Asp	Ser	Lys			
195																	200	
200																	205	
205																		

aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg	672
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	
210 215 220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa	720
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc	768
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	
245 250 255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	
260 265 270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct	864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	
275 280 285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag	912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	
290 295 300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac	960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr	
305 310 315 320	
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg	1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val	
325 330 335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac	1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp	
340 345 350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg	1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val	
355 360 365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca	1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr	
370 375 380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca	1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	
385 390 395 400	
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg	1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	
405 410 415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc	1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	
420 425 430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc	1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile	

435

440

445

ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc 1392
 Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga 1452
 gccgtggact cagctctcac ttccctcag ccccacttgc tggctggct cttgttcagg 1512
 taggctccgc ccggggcccc tggcctcagc atcagccct cagtcctccct gggcacccag 1572
 atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt 1632
 gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtcccatt ctcagctgaa 1692
 atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac 1752
 gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt ccccccgtct 1812
 gagaatgtcc ctggaaggaa gccagttaat aaaccttgggt tggatggaat ttggagagtc 1872

g 1873

<210> 4
 <211> 464
 <212> PRT
 <213> Sus scrofa
 <400> 4

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
 1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Thr Lys Ala
 20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
 35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
450 455 460

<210> 5
<211> 1873
<212> DNA
<213> Sus scrofa

<220>
<221> CDS
<222> (1)..(1392)

<400> 5
atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly
35 40 45

ccg agg gaa agt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

TOP SECRET//NOFORN

gcc gag gtg gac aac ccc cca aca gag cg ^g gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	85	90	95	288	
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	100	105	110	336	
ata gag ttc tca gcc tcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val	115	120	125	384	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	130	135	140	432	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	145	150	155	160	480
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	165	170	175	528	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	180	185	190	576	
gcc ctg gtg gcc aac ggc gtc cga gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys	195	200	205	624	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	210	215	220	672	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	225	230	235	240	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	245	250	255	768	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val	260	265	270	816	
tac gcc ctc atc aag aac ccg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro	275	280	285	864	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag ccg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys	290	295	300	912	
ttc ctg cac atc ttt ggc acc ctg ctg ccc ccg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr				960	

卷之三

305	310	315	320
cgc acc atccaa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val			
325	330	335	1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc ttg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp			
340	345	350	1056
cggtgt tct gct cct gtg gtc aac gaa act gga cag gta ttg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val			
355	360	365	1104
ggc ctc tac tct cgc ttt gat ttg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr			
370	375	380	1152
tac aac cac ctg gac atg aat ttg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr			
385	390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly			
405	410	415	1248
gaa gtc att gac cgg att gtc cgg gaa cag ttg cac cgc ctg gtc ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu			
420	425	430	1296
gtg gat gag acc cag cac ctt ctg ggc ttg ttg tcc ctc tct gac atc Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile			
435	440	445	1344
ctt cag gct ctg ttg ctc agc cct gct gga att gat gcc ctc ggg gcc Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
450	455	460	1392
tgagaacctt ggaacctttt ctctcaggcc acctggcaca cctggaaagcc agtgaaggga			
ggcggtggact cagctctcac ttcccttcag cccacttgc tggctggct cttgttcagg			
taggctccgc ccggggcccc tggcctcagc atcagccccct cagtctccct gggcacccag			
atctcagact ggggcacccct gaagatggga gtggcccagc ttatagctga gcagccttgt			
gaaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtccatt ctcagctgaa			
atgatggagg gcctcataag aggggtggac agggccttgg a tagaggccca gatcagtgac			
gtgccttcag gacctccggg gagtttagagc tgccctctct cagttcagtt ccccccgt			
gagaatgtcc ctgaaaggaa gccagtaat aaaccttggt tggatggaaat ttggagagtc			

<210> 6
<211> 464

<212> PRT
<213> Sus scrofa

<400> 6

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

卷之三

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
 245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
 275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe	Leu	His	Ile	Phe	Gly	Thr	Leu	Leu	Pro	Arg	Pro	Ser	Phe	Leu	Tyr
305				310					315					320	

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala

450

455

460

<210> 7
 <211> 1873
 <212> DNA
 <213> Sus scrofa

<220>
 <221> CDS
 <222> (1)...(1392)

<400> 7
 atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48
 Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
 1 5 10 15

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
 Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
 20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Gly Gly Pro Pro Gly
 35 40 45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
 50 55 60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240
 Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
 65 70 75 80

gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac 288
 Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
 85 90 95

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc 336
 Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
 100 105 110

ata gag ttc tca gcc tcg gcg tcg ggg gat gag ctt ggg ctg gtg 384
 Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val
 115 120 125

gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg 432
 Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
 130 135 140

ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg 480
 Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
 145 150 155 160

cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc 528
 His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
 165 170 175

aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt 576
 Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe

180	185	190	
gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys 195	200	205	624
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val 210	215	220	672
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu 225	230	235	720
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245	250	255	768
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val 260	265	270	816
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro 275	280	285	864
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290	295	300	912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305	310	315	960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325	330	335	1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340	345	350	1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355	360	365	1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370	375	380	1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385	390	395	1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405	410	415	1248
gaa gtc att gac cgg att gtc cgg gaa cag cag gtg cac cgc ctg gtg ctc			1296

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu		
420	425	430
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc		1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile		
435	440	445
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc		1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala		
450	455	460
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaaagcc agtgaaggga		1452
gccgtggact cagctctcac ttccccctcag ccccacttgc tggctggct cttgttcagg		1512
taggctccgc ccggggccccc tggcctcagc atcagccccct cagtctccct gggcacccag		1572
atctcagact ggggcacccct gaagatggga gtggcccgac ttatactgtga gcagccttgt		1632
gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtccatt ctcagctgaa		1692
atgatggagg gcctcataag aggggtggac agggcctggg gtagaggcca gatcagtgc		1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt ccccccgtct		1812
gagaatgtcc ctggaaaggaa gccagttaat aaaccttggg tggatggaaat ttggagagtc		1872
g		1873

<210> 8
<211> 464
<212> PRT
<213> Sus scrofa

<400> 8
Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu
65					70				75						80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val

325

330

335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
 340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
 355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
 370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
 405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
 420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
 435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
 450 455 460

<210> 9
 <211> 1873
 <212> DNA
 <213> Sus scrofa

<220>
 <221> CDS
 <222> (1)...(1392)

<400> 9
 atg agc ttc cta gag caa gga gag agc cgt tca tgg cca tcc cga gct 48
 Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
 1 5 10 15

gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96
 Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
 20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144
 Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
 35 40 45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192
 Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln

卷之三

50	55	60	
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu			
65	70	75	80
240			
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp			
85	90	95	288
tgc gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
100	105	110	336
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val			
115	120	125	384
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg			
130	135	140	432
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met			
145	150	155	160
540			
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser			
165	170	175	528
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe			
180	185	190	576
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys			
195	200	205	624
672			
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val			
210	215	220	720
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu			
225	230	235	240
768			
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe			
245	250	255	816
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val			
260	265	270	864
912			
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro			
275	280	285	912
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag ccg ctt ctc aag			

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys			
290	295	300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac			960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr			
305	310	315	320
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg			1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val			
325	330	335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac			1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp			
340	345	350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg			1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val			
355	360	365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca			1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr			
370	375	380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca			1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr			
385	390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg			1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly			
405	410	415	
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc			1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu			
420	425	430	
gtg gat gag acc cag cac ctt ctg ggc gtg tcc ctc tct gac atc			1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile			
435	440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc			1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
450	455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca ccttggagcc agtgaaggga			1452
gccgtggact cagctctcac ttcccctcag ccccacttgc tggctggct cttgttcagg			1512
taggctccgc ccggggcccc tggcctcagc atcagccccct cagtcctccct gggcacccag			1572
atctcagact ggggcacccct gaagatggga gtggcccagc ttatagctga gcagccttgt			1632
gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtcccatt ctcagctgaa			1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac			1752
gtgccttcag gacctccggg gagtttagagc tgccctctct cagttcagtt ccccccgtct			1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttgggt tggatggaat ttggagagtc			1872

<210> 10
<211> 464
<212> PRT
<213> Sus scrofa

<400> 10

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe
180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys

195

200

205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala
450 455 460

<210> 11
<211> 1095
<212> DNA
<213> Sus scrofa

<400> 11
gaaactcttc tccccacaga ctccctcctg gagcagcctc gggggaccta agcatcaagg 60
taggtggggc tgccctgct cgcgccca ggctcttctc ccacccctt ttcttccacg 120
tcttcaggac cccaatctcc cccactccac tcgcctggct cttgtttcc tctcctttgc 180
cttctttgtt ccgctttgtt tcttcttcct ccctctccct cacccctccct ctctttcaaa 240
agagtagagg gggcatctat agagtctgga gattggact ctcttgactt tctcgcttac 300
tagctgtgtg atttgtggca aattgcttca cctctctgag ctcaaggctc tcgttagtaa 360
aacagggctg atagccatgc cttcggata agattgccgt gaggggtgaa tgagaaattt 420
gttggaggac aagccctttg aagcttccca atattaaata tttttattta ttttattttt 480
ttttgtcttt ttgctattcc tttggggccgc tcccacggca tatggaggtt cccaggctag 540
gggtcgaatc ggagctgttag ccactggct acgccagagc cacagcaacg cgggatccga 600
gccgcacatctg caacctacac cacagctcac ggcaacgccc gatcgtaac ccactgagca 660
ggggcaggca ccgaacctgc aacctcatgg ttcctagtg gattcgtaa ccactgcgcc 720
acgacggaa ctccccata ttaaatatta ttatttagtaa catttaatg gaatttattg 780
tgttactccc cattaaccaa acaggtcccc ttctccctt cagagatgag ctccctagag 840
caaggagaga gccgttcatg gccatccca gctgtgacca ccagctcaga aagaagccat 900
ggggaccagg ggaccaaggc ctctagatgg acaaggcagg aggatrtaga ggaagggggg 960
cctccgggccc cgagggaaarg tgagttcaag gccagttctg gggagctggg actggggca 1020
gtgggcagtc ctcaaacctg gggccgtct ctggcttgtt ccctccataa cacaggcaca 1080
taacatcatg cagcc 1095

<210> 12
<211> 808
<212> DNA
<213> Sus scrofa

<400> 12

gaaactttc tccccacaga ctccctctg gagcagccctc gggggaccta agcatcaagg	60
taggtggggc tgccccctgct cgcccccca ggctttctc ccacccctt ttcttcacg	120
tcttcaggac cccaatctcc cccactccac tcgcctggct cttgtcttcc tctccttgc	180
cttcttgtt ccgctttgtt tcttcttctt ccctctccct cacccctcc ctcttcaaa	240
agagtagagg gggcatctat agagtctgga gattggact ctcttgactt tctcgcttac	300
tagctgtgtg atttgtggca aattgtttca cctctctgag ctcaggtctc tcgttagtaa	360
aacagggctg atagccatgc cttcggata agattgccgt gagggttgaa tgagaaattt	420
gttggaggac aagccctttg aagcttcca atattaaata ttattattag taacatttta	480
atggaattta ttgtgttact cccattaac caaacaggtc ccattctccc ttgcagagat	540
gagcttccta gagcaaggag agagccgttc atggccatcc cgagctgtga ccaccagctc	600
agaaagaagc catggggacc aggggaccaa ggcctctaga tggacaaggc aggaggat	660
agaggaaggg gggcctccgg gcccggggaa argtgagttc aaggccagtt ctggggagct	720
gggactgggg gcagtgggca gtcctaaac ctggggcccg tctctggtct ggtccctcca	780
taacacaggc acataaacatc atgcagcc	808

<210> 13
<211> 21
<212> DNA
<213> Sus scrofa

<400> 13
atgagcttcc tagagcaagg a

21

<210> 14
<211> 22
<212> DNA
<213> Sus scrofa

<400> 14
ggctgcatga tgttatgtgc ct

22

<210> 15
<211> 21
<212> DNA
<213> Sus scrofa

<400> 15
gaaactttc tccccacaga c

21

<210> 16
<211> 20
<212> DNA

<213> Sus scrofa

<400> 16

ggagcaaatg tgcagacaag

20

<210> 17

<211> 20

<212> DNA

<213> Sus scrofa

<400> 17

cccacgaagc tctgcttctt

20